Conclusions: Correlation between gut bacterial compositions and parasitic infection in Malaysian adolescence was detected. Nevertheless, disentangling the relationship between the infection and the gut microbiota dynamic is difficult due to the confounding lifestyle and diet difference. Notwithstandingly, our results provided baseline information to facilitate further study on the interaction between gut microbiota and helminth colonisation.

OS 8-4

DEVELOPMENT THE DETECTION METHOD OF *SARCOCYSTIS* DNA FROM STOOL SPECIMEN AS THE PROOF FOR FOODBORNE CASES

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Purpose: Sarcocystosis is parasitic infectious disease caused by protozoan apicomplexan parasite of the genus *Sarcocystis*. *Sarcocystis* are globally distributed, and have a two-host cycle, generally with carnivores or omnivores as definitive hosts (DH) and herbivores as intermediate hosts (IH). Humans can serve as definitive hosts for *S. hominis* and *S. suihominis* after eating raw meat from cattle and pig, respectively. In Japanese cuisine, raw horse meat is known as "Basashi", and it is popular in some regions of Japan. To date, "Basashi" has been known as safe food from the risk of contamination by parasite compared with raw beef meat or raw pork meat. However, between 2009, June and 2014, Jan., 48 cases of gastroenteritis with unknown sources, but ate raw horse meat was reported. Since *Sarcocystis fayeri* was reported as possibly the causative agent, the issue on food safety for consumption of raw horse meat has been concerned.
To prove the food poisoning, the evidence from both of food and patient is important, but suspicious meat sample is not always remained, thus testing meat if it contain infectious agents is difficult. In this study, to develop an alternative tool is focused on to investigate parasitic DNA that might be contained in stool of patients when the leftover raw horse meat is not available.
Methods: Using spike experiment with genomic DNA of *Sarcocystis* sp. and bradyzoites originally obtained from sarcocyst in horse meat, try to detect the parasitic DNA from stool specimens derived from a patient who is obviously not associated with any food poisoning cases. Recombinant plasmid DNA contained target region of *S. fayeri*. 18S rRNA gene was used to spike experiment and to detect parasitic DNA from stool samples, nested PCR was carried out.
Results: Specific bands of spiked 10^4 copies of plasmid DNA containing 18S rRNA genes of *S. fayeri* was identified with gel electrophoresis under the UV- transilluminator.
Conclusions: When the leftover meat is not available, detection of specific DNA for *Sarcocystis* sp. from stool specimens derived from patients who is involved with gastroenteritis can be useful. This method can be used as diagnostic tool to investigate foodborne cases that is responsible for eating raw horse meat.

OS 8-5

SYSTEM BIOLOGY ANALYSES OF THE DYNAMIC HOST RESPONSE TO *TOXOPLASMA GONDII* INFECTION IN A MURINE MODEL

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Purpose: Toxoplasmosis, one of the most common parasitic diseases worldwide, is caused by the protozoan *Toxoplasma gondii*. It is a parasite with no specific host and has more than one obligatory host in its life cycle. *T. gondii* is prevalent in most part of the world with an estimated one third of the global human population infected. Thus, it is imperative that the mechanism of infection and the interactions between parasite and mammalian host are elucidated to uncover the mechanisms of pathology ultimately leading to improved disease diagnosis, control and surveillance. Here, we compared the serum cytokines, urine metabolite and faecal bacterial profiles of mice infected with *T. gondii* using integrated systems biology approach to assess and unravel the complex interactions between the host and the parasite. *T. gondii* infection led to up-regulation of serum cytokine levels which correlated with perturbations in urinary metabolites and faecal bacteria compositions.
Methods: Murine model of T. gondii infection was established and the tissue, urine, blood serum and faecal pellet were harvested for analyses. Infection was assessed by histopathology of brain slices using H & E staining. Subsequent serum, urine and faecal samples were analysed using multiplex, nuclear magnetic resonance spectroscopy and TRFLP respectively. The data generated were analysed using multivariate statistical analysis and the covariation between the cytokines, NMR data and bacteria populations were explored using correlation network analyses and multiple linear regressions modelling techniques.
Results: The integrated systems biology approach using correlation network analyses of data from the three matrices showed differences in energy metabolism and gut microbe metabolism, distinctive immunological phenotypes, and shifts in microbial composition between the infected and control animals.

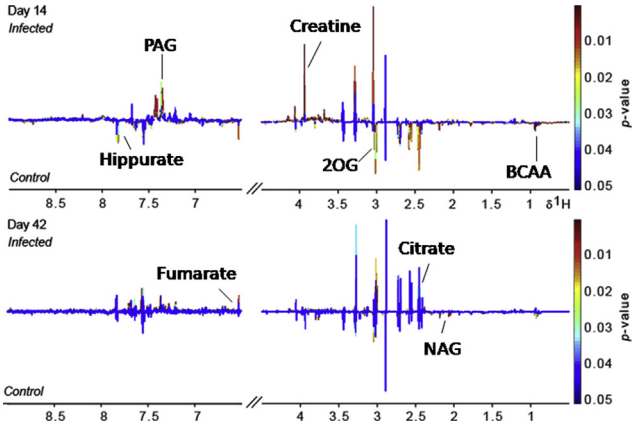

Fig 1 Urinary ^{1}H NMR-derived differential metabogram showing significant metabolic differences between control and infected animals on days 14 and 42.

Conclusions: The current study showed complex interactions between the host and the parasites across the three biological compartments. The correlation between host innate immune response, host metabolism and gut microbiome were established. This study proved that *T. gondii* infection will affect not only host physiological functions but the host gut microbiome as well. Results from the current study enhance understanding of parasite infection in mammalian system and facilitate biomarkers discovery.

OS 8-6

INCRIMINATION OF *ANOPHELES BALABACENSIS* AS THE VECTOR FOR SIMIAN MALARIA IN KUDAT DIVISION, SABAH, MALAYSIA.

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Purpose: *Plasmodium knowlesi* is a simian malaria parasite affecting humans, leading to fatal infections in Sabah. High number of cases was reported from the Kudat Division. A 12 months study was performed to identify the simian malaria vectors.